Ion C. Baianu and James F. Glazebrook

Quantum Nano-Automata and Life's MV- Logics

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Abstract   A novel approach to gene and neural networks, as well interactomics, in terms of quantum nano-automata formally represented in a categorical and Lukasiewicz-Topos framework of Lukasiewicz-Moisil (LM) Algebraic, many-valued (MV) Logics. General models of nonlinear dynamics in complex functional systems such as neural networks, genomes and cell interactomes are proposed based on categories of interacting quantum automata. Specific realizations of such LM-Algebraic Logic models of genetic networks and signaling pathways in cells are formulated in terms of categories of variable graphs and pseudographs of N-state components that allow for the generalization of previous logical models of both genetic activities and neural networks. An algebraic formulation of variable 'next-state functions' is extended to a Lukasiewicz Topos with an N-valued LM Algebraic Logic subobject classifier description that represents non-random and nonlinear network activities as well as their transformations in highly-complex processes, such as morphogenesis, develeopment, ageing and carcinogenesis.

1.1   Introduction

The concepts of quantum automata and quantum computation are studied in the context of quantum genetics and genetic networks with nonlinear dynamics. In a previous publication (Baianu,1971a) the formal concept of quantum automaton was introduced and its possible implications for genetic and metabolic activities in living cells and organisms were considered. This was followed by a report on quantum and abstract, symbolic computation based on the theory of categories, functors and natural transformations (Baianu,1971b). The notions of topological semigroup, quantum automaton,or quantum computer, were then suggested with a view to their potential applications to the analogous simulation of biological systems, and especially genetic activities and nonlinear dynamics in genetic networks. Further, detailed studies of nonlinear dynamics in genetic networks were carried out in categories of n-valued, Lukasiewicz Logic Algebras that showed significant dissimilarities

(Baianu, 1977) from Bolean models of human neural networks (McCullough and Pitts,1945). Molecular models in terms of categories, functors and natural transformations were then formulated for uni-molecular chemical transformations, multi-molecular chemical and biochemical transformations (Baianu, 1983,2004a). Previous applications of computer modeling, classical automata theory, and relational biology to molecular biology, oncogenesis and medicine were extensively reviewed and several important conclusions were reached regarding both the potential and limitations of the computation-assisted modeling of biological systems, and especially complex organisms such as Homo sapiens sapiens(Baianu,1987). Novel approaches to solving the realization problems of Relational Biology models in Complex System Biology are introduced in terms of natural transformations between functors of such molecular categories. Several applications of such natural transformations of functors were then presented to protein biosynthesis, embryogenesis and nuclear transplant experiments. Other possible realizations in Molecular Biology and Relational Biology of Organisms are here suggested in terms of quantum automata models of Quantum Genetics and Interactomics. Future developments of this novel approach are likely to also include: Fuzzy Relations in Biology and Epigenomics, Relational Biology modeling of Complex Immunological and Hormonal regulatory systems, n-categories and Topoi of Lukasiewicz Logic Algebras and Intuitionistic Logic (Heyting) Algebras for modeling nonlinear dynamics and cognitive processes in complex neural networks that are present in the human brain, as well as stochastic modeling of genetic networks in Lukasiewicz Logic Algebras.

1.1.1   Background

1.1.1.1   The Concepts of Quantum Automata and Quantum Dynamics in terms of the Theory of Categories, Functors and Natural Transformations

It is often assumed incorrectly that Quantum Computation was introduced in 1982. There are also numerous citations of Quantum Automata papers printed in the late 80s and recent quantum computation textbooks also fail to report the first introduction of the concept of quantum automaton. Quantum Computation and Quantum Automata were introduced in 1971 in a paper published in the Bulletin of Mathematical Biophysics, 33:339-354 (Baianu, 1971a). Categorical computations, both algebraic and topological, were also introduced the same year based on adjoint functor pairs in the theory of categories, functors and natural transformations (Baianu, 1971b). The notions of topological semigroup, quantum automaton,or computer, were then suggested with a view to their potential applications to the analogous simulation of biological systems, and especially genetic activities and nonlinear dynamics in geneticnetworks. Further, detailed studies of nonlinear dynamics in genetic networks were carried out in categories of n-valued, Lukasiewicz Logic Alge-

bras that showed significant dissimilarities (Baianu, 1977) from Bolean models of human neural networks (McCullough and Pitts, 1945). Molecular models in terms of categories, functors and natural transformations were then formulated for uni-molecular chemical transformations, multi-molecular chemical and biochemical transformations (Baianu, 1983, 2004a). Previous applications of computer modeling, classical automata theory, and relational biology to molecular biology, oncogenesis and medicine were extensively reviewed and several important conclusions were reached regarding both the potential and limitations of the computation-assisted modeling of biological systems, and especially complex organisms such as Homo sapiens sapiens (Baianu,1987).

1.1.2   'Fuzzy' Logics of Living Organisms

Living organisms or biosystems can be represented as super-complex systems with dynamics that is not reducible to that of their components, such as molecules and atoms. It is an empirically accepted fact that living organisms exhibit a wide degree of 'biological variability': genetic, epigenetic and also phenotypic, metabolic within the same species; their behavior and dynamics thus exhibit a type of 'fuzziness' (refs.[31, 33]) that unlike Zadeh's fuzzy sets characteristic ([47, 48]) is neither random nor always following a (symmetric) Gaussian distribution. It has been proposed that the operational logics underlying super-complex systems are LM_N many-valued logics of different types for both genetic and neural networks (refs. [33, 45]).

1.2   Quantum Automaton and Quantum Computation

Quantum computation and quantum 'machines' (or nanobots) were much publicized in the early 1980's by Richard Feynman (Nobel laureate in Physics),and, subsequently, a very large number of papers were published on this topic by a rapidly growing number of quantum theoreticians and applied mathematicians.

DEFINITION 1.1   *A quantum automaton Q_A can be simply defined as* an extension of an automaton with quantum states instead of the sequentially determined states, inputs and outputs of a *sequential, or state machine*.

The precise mathematical definitions of quantum automaton, variable automaton, and quantum computation were first introduced formally in refs. [1] and [2] in relation to relational models in Quantum Relational Biology (*loc.cit*).

DEFINITION 1.2

One obtains a simple definition of *quantum automaton* by considering instead of the transition function of a classical sequential machine, the (quantum) transitions in a finite quantum system with definite probabilities determined by quantum dynamics. The *quantum state space* of a *quantum automaton* is thus defined as a quantum groupoid over a bundle of Hilbert spaces, or over rigged Hilbert spaces. Formally, whereas a sequential machine, or state machine with state space S, input set I and output set O, is defined as a quintuple: $(S, I, O, \delta : S \times S \to S, \lambda : S \times I \to O)$, a *quantum automaton* is defined by a triple $(H, \Delta : H \to H, \mu)$, where H is either a Hilbert space or a rigged Hilbert space of quantum states and operators acting on H, and μ is a measure related to the quantum logic, LM, and (quantum) transition probabilities of this quantum system.

REMARK 1.1   Quantum 'computation' becomes possible only when macroscopic blocks of quantum states can be controlled *via* quantum preparation and subsequent, classical observation. Obstructions to 'building', or constructing quantum computers are known to exist in dimensions greater than 2 as a result of the standard K-S theorem. Subsequent definitions of quantum computers reflect attempts to either avoid or surmount such difficulties often without seeking solutions through quantum operator algebras and their representations related to extended quantum symmetries which define fundamental invariants that are key ▊

DEFINITION 1.3   Alternatively, as a quantum algebraic topology object,

a *quantum automaton* is defined by the triplet $(\mathbb{G}, H - \Re_{\mathbb{G}}, Aut(\mathbb{G}))$, where $\mathbb{G}$ is a locally compact *quantum groupoid*, H-$\Re_{\mathbb{G}}$ are the unitary representations of $\mathbb{G}$ on rigged Hilbert spaces $\Re_{\mathbb{G}}$ of quantum states and quantum operators on H, and $Aut(\mathbb{G})$ is the transformation, or automorphism, groupoid of quantum transitions.

REMARK 1.2   Other definitions of quantum automata and quantum computations have also been reported that are closely related to recent experimental attempts at constructing quantum computing devices.   ▊

Two examples of such definitions are briefly considered next.

DEFINITION 1.4   *Quantum automata* were defined in refs.[1] and [2] as

generalized, probabilistic automata with quantum state spaces. Their next-state functions operate through transitions between quantum states defined by the quantum equations of motions in the Schrödinger representation, with both initial and boundary conditions in space-time.

A new theorem was proven which states that the *category of quantum au-*

tomata and automata–homomorphisms has both limits and colimits. There-fore, both categories of quantum automata and classical automata (sequential machines) are *bicomplete.* A second new theorem established that the standard automata category is a subcategory of the quantum automata category.

1.2.1 Related Results: Quantum Automata Applications to Modeling Complex Systems.

The quantum automata category has a faithful representation in the category of Generalized (M, R) -systems which are open, dynamic bio-networks ([**?**]) with defined biological relations that represent physiological functions of primordial(s), single cells and the simpler organisms. A new *category of quantum computers* is also defined in terms of *reversible* quantum automata with quantum state spaces represented by topological groupoids that admit a local characterization through unique 'quantum' *Lie algebroids.* On the other hand, the category of n-Lukasiewicz algebras has a subcategory of *centered n-* Lukasiewicz algebras [15] (which can be employed to design and construct subcategories of quantum automata based on n-Lukasiewicz diagrams of existing VLSI. Furthermore, as shown in ref.([15] the category of centered n-Lukasiewicz algebras and the category of Boolean algebras are naturally equivalent.

Variable machines with a varying transition function were previously discussed informally by Norbert Wiener as a possible model for complex biological systems although how this might be achieved in *Biocybernetics* has not been specifcally, or mathematically presented by Wiener.

A 'no-go' conjecture was also proposed which states that Generalized (**M,R**)–Systems complexity prevents their complete computability by either standard or quantum automata. The concepts of quantum automata and quantum computation were initially studied and are also currently further investigated in the contexts of quantum genetics, genetic networks with nonlinear dynamics, and bioinformatics. In a previous publication (ICB71a)– after introducing the formal concept of quantum automaton–the possible implications of this concept for correctly modeling genetic and metabolic activities in living cells and organisms were also considered. This was followed by a formal report on quantum and abstract, symbolic computation based on the theory of categories, functors and natural transformations [2]. The notions of topological semigroup, quantum automaton,or quantum computer, were then suggested with a view to their potential applications to the analogous simulation of biological systems, and especially genetic activities and nonlinear dynamics in genetic networks. Further, detailed studies of nonlinear dynamics in genetic networks were carried out in categories of n-valued, Lukasiewicz Logic Algebras that showed significant dissimilarities [33] from the widespread Bolean models of human neural networks that may have begun with the early publication of [16]. Molecular models in terms of categories, functors and natural transformations were then formulated for uni-molecular chemical transforma-

tions, multi-molecular chemical and biochemical transformations [**?**]. Previous applications of computer modeling, classical automata theory, and relational biology to molecular biology, oncogenesis and medicine were extensively reviewed and several important conclusions were reached regarding both the potential and limitations of the computation-assisted modeling of biological systems, and especially complex organisms such as *Homo sapiens sapiens* [**?**]. Novel approaches to solving the realization problems of Relational Biology models in Complex System Biology are introduced in terms of natural transformations between functors of such molecular categories. Several applications of such natural transformations of functors were then presented to protein biosynthesis, embryogenesis and nuclear transplant experiments. Other possible realizations in Molecular Biology and Relational Biology of Organisms were then suggested in terms of quantum automata models of Quantum Genetics and Interactomics. Future developments of this novel approach are likely to also include: Fuzzy Relations in Biology and Epigenomics, Relational Biology modeling of Complex Immunological and Hormonal regulatory systems, n-categories and *generalized LM*–Topoi of Lukasiewicz Logic Algebras and intuitionistic logic (Heyting) algebras for modeling nonlinear dynamics and cognitive processes in complex neural networks that are present in the human brain, as well as stochastic modeling of genetic networks in Lukasiewicz Logic Algebras (LLA).

1.2.2   Quantum Automata, Quantum Computation and Quantum Dynamics Represented by Categories, Functors and Natural Transformations.

Molecular models were previously defined in terms of categories, functors and natural transformations were formulated for unimolecular chemical transformations, multi-molecular chemical and biochemical transformations [45]. Dynamic similarities or analogies between categories of classical, quantum or complex systems and their transformations were then naturally represented in terms of adjoint functors and the corresponding natural equivalences.

REMARK 1.3   . Previous applications of computer modeling, classical automata theory, and relational biology to molecular biology, neural networks, oncogenesis and medicine were extensively reviewed in a previous monograph and several important conclusions were reached regarding both the potential and the severe limitations of the algorithm driven, recursive computation-assisted modeling of complex biological systems [11]. ▌

1.3 Quantum Nano-Automata and Quantum Computation Theorems

Quantum computation and quantum 'machines' (or nanobots) were much publicized in the early 1980's by Richard Feynman (Nobel Laureate in Physics for his approach to Quantum Electrodynamics, or QED), and subsequently a very large number of papers were published on this topic by a rapidly growing number of quantum theoreticians and some applied mathematicians. Two such specific definitions of QAs are briefly considered next.

Quantum automata were defined in refs. [2] and [3] as *generalized, probabilistic automata with quantum state spaces*. Their next-state functions operate through transitions between quantum states defined by the quantum equations of motions in the Schrödinger representation, with both initial and boundary conditions in space-time. Such quantum automata are here renamed as *S-quantum automata*.

DEFINITION 1.5

One obtains a simple, formal definition of *an S-quantum automaton*, that is a quantum automaton with *a quantum state space*, by considering instead of the transition function of a classical sequential machine, the (quantum) transitions in a finite quantum system with definite probabilities determined by quantum dynamics. The *quantum state space* of *an S-quantum automaton* is thus defined as a quantum groupoid over a bundle of Hilbert spaces, or over rigged Hilbert spaces. Whereas a sequential machine, or state machine with state space S, input set I and output set O, is defined as a quintuple: $(S, I, O, \delta : S \times S \to S, \lambda : S \times I \to O)$, *an S- quantum automaton* is precisely defined by a triple $(H, \Delta : H \to H, \mu)$, where H is either a Hilbert space or a rigged Hilbert space of quantum states and operators acting on H, and μ is a measure related to the quantum logic, LM, and (quantum) transition probabilities of this quantum system.

Two new theorems are also noted in this context (albeit stated here without proof):

THEOREM 1.1

Bicompleteness Theorem. *The category of S-quantum automata and S-quantum automata homomorphisms has both limits and colimits.*

THEOREM 1.2

Classical Embedding Theorem. *The category of classical, finite automata is a subcategory of the category of S-quantum automata.*

Therefore, both categories of S-quantum automata and classical automata (sequential machines) are *bicomplete* as **Theorem 3** states that the standard automata category, C_{SA}, is a subcategory of the S-quantum automata category, C_{QA}, or in shorthand notation: $C_{SA} \prec C_{QA}$.

REMARK 1.4   Quantum computation becomes possible only when macroscopic blocks of quantum states can be controlled *via* quantum preparation and subsequent, classical observation. Obstructions to actually building, or constructing quantum computers are known to exist in dimensions greater than 2 as a result of the standard **K-S** theorem. Subsequent definitions of quantum computers reflect attempts to either avoid or surmount such difficulties often without seeking solutions through quantum operator algebras and their representations related to extended quantum symmetries which define fundamental invariants that are key to actual constructions of this type of quantum computers. ∎

Defining a quantum automaton as an object of a Quantum Algebraic Topology (QAT) theory requires the concept of *quantum groupoid* (or of a weak Hopf algebra) which is defined as follows.

DEFINITION 1.6   Quantum groupoids, Q_{Gd}'s, are currently defined *either as quantized, locally compact groupoids endowed with a left Haar measure system,* (Gd, μ), *or as* weak Hopf algebras *(WHA). This concept can also be considered as an extension of the notion of quantum group, which is sometimes represented by a Hopf algebra,* H.

The concept of Hopf algebra, or 'quantum group', will be introduced next in three steps.

DEFINITION 1.7   *Firstly, an* unital associative algebra *consists of a linear space A together with two linear maps*

$$m : A \otimes A \to A \;\; \text{(multiplication)}, \;\; \eta : \mathbf{C} \to A \;\; \text{(unity)}, \qquad (1.1)$$

satisfying the conditions

$$m(m \otimes \mathbf{1}) = m(\mathbf{1} \otimes m), \qquad (1.2)$$

and

$$m(\mathbf{1} \otimes \eta) = m(\eta \otimes \mathbf{1}) = \mathrm{id}. \qquad (1.3)$$

Next let us consider 'reversing the arrows', and take an algebra A equipped with a linear homorphisms $\Delta : A \to A \otimes A$, *satisfying, for* $a, b \in A$:

$$\Delta(ab) = \Delta(a)\Delta(b), \qquad (1.4)$$

$$(\Delta \otimes \mathrm{id})\Delta = (\mathrm{id} \otimes \Delta)\Delta. \qquad (1.5)$$

We call Δ *a* comultiplication, *which is said to be* coassociative. *There is also a counterpart to* η, *the* counity *map* $\epsilon : A \to \mathbf{C}$ *satisfying*

$$(\mathrm{id} \otimes \epsilon) \circ \Delta = (\epsilon \otimes \mathrm{id}) \circ \Delta = \mathrm{id}. \qquad (1.6)$$

DEFINITION 1.8   *A* bialgebra $(A, m, \Delta, \eta, \epsilon)$ *is defined as a linear space* A *with maps* m, Δ, η, ϵ *satisfying the above properties.*

Now, in order to recover anything resembling a group structure, one must append such a bialgebra with an antihomomorphism $S : A \to A$, *satisfying*

$$S(ab) = S(b)S(a), \qquad (1.7)$$

for $a, b \in A$. *This map is defined implicitly via the property:*

$$m(S \otimes \mathrm{id} \circ \Delta) = m(\mathrm{id} \otimes S) \circ \Delta = \eta \circ \epsilon \qquad (1.8)$$

We call S *the* antipode map.

DEFINITION 1.9   *A* Hopf algebra *is then defined as a bialgebra* $(A, m, \eta, \Delta, \epsilon)$ *equipped with an antipode map* S.

Commutative and non-commutative Hopf algebras form the backbone of quantum groups [17],[23], [24], and are thus essential to the generalizations of symmetry. Indeed, in most respects a quantum group is identifiable with a Hopf algebra. When such algebras are actually associated with proper groups of matrices there is considerable scope for their representations on both finite and infinite dimensional Hilbert spaces.

Alternatively, as defined in refs.[17],[23] quantum groupoids can be regarded simply as *weak Hopf algebras*. Algebroid symmetries, on the other hand, figure prominently both in the theory of dynamical deformations of quantum 'groups' (e.g., Hopf algebras) and the quantum Yang–Baxter equations.

DEFINITION 1.10   *In order to define a* weak Hopf algebra, *one can relax certain axioms of a Hopf algebra as follows:*

(1) *The comultiplication is not necessarily unit-preserving.*

(2) *The counit* ϵ *is not necessarily a homomorphism of algebras.*

(3) *The axioms for the antipode map* $S : A \to A$ *with respect to the counit are as follows. For all* $h \in H$,

$$m(\mathrm{id} \otimes S)\Delta(h) = (\epsilon \otimes \mathrm{id})(\Delta(1)(h \otimes 1)), \qquad (1.9)$$

$$m(S \otimes \mathrm{id})\Delta(h) = (\mathrm{id} \otimes \epsilon)((1 \otimes h)\Delta(1)), \qquad (1.10)$$

$$S(h) = S(h_{(1)})S(h_{(2)})S(h_{(3)}) \qquad (1.11)$$

Several authors substitute the term *quantum groupoid* for a weak Hopf algebra, although this algebra in itself is not a proper groupoid, but it may have a component *group* algebra as in certain examples of the quantum double; nevertheless, weak Hopf algebras generalise Hopf algebras that, with additional properties, were previously introduced as' quantum groups' by mathematical physicists.

Note, however, that the requirement of *local compactness* for quantum groupoids, as well as that of the existence of a left Haar measure system, is not generally considered for quantum groups. *Quantum groupoid representations* can thus define extended quantum symmetries beyond the 'Standard Model' (SUSY) in Mathematical Physics or Noncommutative Geometry.

DEFINITION 1.11   An *algebraic quantum automaton*, or *A-quantum automaton* can now be defined as a quantum algebraic topology object– the triplet

$$Q_A = (G_d, H - R_{G_d}, Aut(G)), \qquad (1.12)$$

where G_d is a locally compact *quantum groupoid*, $H - R_{G_d}$ are the unitary representations of G_d on rigged Hilbert spaces R_{G_d} of quantum states and quantum operators on H, and $Aut(G_d)$ is the transformation, or automorphism, groupoid of quantum transitions that represents all flip-flop quantum transitions of one qubit each between the permitted quantum states of the quantum automaton*.

REMARK 1.5   Other definitions of quantum automata and quantum computations have also been reported that are closely related to recent experimental attempts at constructing quantum computing devices. One can consider next the *category of quantum automata.* ▮

DEFINITION 1.12   The *category of algebraic quantum automata* C_{QA} is defined as an algebraic category whose objects are *A*-quantum automata defined by triples $(H, \Delta : H \to H, \mu)$ (where H is either a Hilbert space or a rigged Hilbert space of quantum states and operators acting on H, and μ is a measure related to the quantum logic, LM, and (quantum) transition probabilities of this quantum system, and whose morphisms are defined between such triples by homomorphisms of Hilbert spaces, $\Delta : H \to H$, naturally compatible with the operators Δ, and by homomorphisms between the associated Haar measure systems.

An alternative definition is also possible based on *Quantum Algebraic Topology*.

DEFINITION 1.13   A *quantum algebraic topology* definition of the *category of algebraic quantum automata C_{QA}* involves the objects specified above in **Definition 4** as *A*-quantum automaton triples (Q_A), and quantum automata homomorphisms defined between such triples; these Q_A morphisms are defined by groupoid homomorphisms $h : Gd \to Gd^*$ and $\alpha : Aut(Gd) \to Aut(Gd^*)$, together with unitarity preserving mappings u between unitary representations of Gd on rigged Hilbert spaces (or Hilbert space bundles).

Quantum-Algebraic Bicompleteness Conjecture.   *The category of A-quantum automata and A-quantum automata homomorphisms has both limits and colimits.*

With these definitions we can now turn to the question of how one can apply quantum automata to modelling problems of highly complex systems and Complex Systems Biology.

1.4   Quantum Automata Applications to Modeling Highly-Complex Systems

One finds that the quantum automata category has a faithful representation in the category of generalised (M, R) -systems (GMRs) which are open, dynamic bio-networks [6] with defined biological relations that represent physiological functions of primordial(s), single cells and higher organisms. A new *category of quantum computers*, C_{QC}, can also be defined in terms of *reversible* quantum automata with quantum state spaces represented by topological groupoids that admit a local characterization through unique 'quantum' *Lie algebroids*. On the other hand, the category of n-Lukasiewicz algebras has a subcategory of *centered n-* Lukasiewicz algebras [15] (which can be employed to design and construct subcategories of quantum automata based on n-Lukasiewicz diagrams of existing VLSI. Furthermore, as shown in ref. [15] the category of centered n-Lukasiewicz algebras and the category of Boolean algebras are naturally equivalent.

Variable machines with a varying transition function were previously discussed informally by Norbert Wiener as possible models for complex biological systems although how this might be achieved in *Biocybernetics* has not been specifcally, or mathematically, presented by Wiener. Therefore, let us consider the formal definitions of simple (M, R)-systems and their generalisations. The simplest MR-system is a relational model of the primordial organism which is defined by the following *categorical sequence (or diagram) of sets and set-*

theoretical mappings: $f : A \to B$, $\phi : B \to \mathrm{Hom}_{MR}(A, B)$, where A is the set of inputs to the MR-system, B is the set of its outputs, and ϕ is the 're-pair map', or R-component, of the MR-system which associates to a certain product, or output b, the 'metabolic' component (such as an enzyme, E, for example) represented by the set-theoretical mapping f. Then, $\mathrm{Hom}_{MR}(A, B)$ is defined as the set of all such metabolic (set-theoretical) mappings (occasionally written incorrectly by some authors as $\{f\}$).

Definition 10. A *general (M, R)-system* was defined by Rosen (1958a,b) as the network or graph of the metabolic and repair components of the type specified specified above in the definition of a simple (M, R) -system; such components are networked in a complex, abstract 'organism' defined by all the abstract relations and connecting maps between the sets specifying all the metabolic and repair components of such a general, abstract model of the biological organism. The mappings between (M, R)-systems are defined as the the metabolic and repair set-theoretical mappings, such as f and ϕ (as specified in the definition of a simple (M, R) -system); moreover, there is also a finite number of sets (just like A and B, respectively, the input and output sets, that are present in the definition of a simple (M, R) -system): A_i, B_i, where $f_i \in \mathrm{Hom}_{MR_i}(A_i, B_i)$ and $\phi \in \mathrm{Hom}_{MR_i}[B, \mathrm{Hom}_{MR_i}(A_i, B_i)]$, with $i \in I$, and I being a finite index set, or directed set, for a a finite number n of distinct metabolic and repair components pairs (f_i, ϕ_i). Alternatively, one may think of a general MR-system as consisting of a finite number N of inter–connected metabolic-repair,MR_i, modules, each one such MR_i module having the input sets A_i and output sets B_i, with $i = 1, 2, ..., n$ being finite integers. To sum up: a *general MR-system* can be defined as a *family of n inter–connected quartets*: $\{(A_i, B_i, f_i, \phi_i)\}_{i \in I}$, where I is an index set of finite integers $i = 1, 2, ..., n$.

With these concepts available we can now turn to defining the category of (M, R)–systems, $\mathbf{C}_{MR}$.

DEFINITION 1.14

A category $\mathbf{C}_{MR}$ of (M, R)-system quartet modules, $\{(A_i, B_i, f_i, \phi_i)\}_{i \in I}$, with I being an index set of integers $i = 1, 2, ..., n$, is a small category of sets with set-theoretical mappings defined by the (M, R)-morphisms between the quarted modules $\{(A_i, B_i, f_i, \phi_i)\}_{i \in I}$, and also with repair components defined as $\phi_i \in \mathrm{Hom}_{MR_i}[B, \mathrm{Hom}_{MR_i}(A_i, B_i)]$, where the (M, R)-morphism composition is defined by the usual composition of functions between sets.

With a few, additional notational changes it can be shown that the category of (M, R)-systems is a subcategory of the category of automata (or sequential machines), $\mathcal{S}_{[M,A]}$. Similar conclusions were also reached independently in ref. [22]. Moreover, one has the following important property of the category $\mathbf{C}_{MR}$ of simple (M, R)-systems.

THEOREM 1.3

(M, R)-**Systems Category Theorem (Baianu, 1973 in ref.** [4]**.** *The category* $\mathbf{C}_{MR}$ *of simple* (M, R)*-systems and their homomorphisms is Cartesian closed.*

REMARK 1.6 Thus, the category $\mathbf{C}_{MR}$ of simple (M, R)-systems belongs to the important family of categories that are Cartesian closed, which also includes the category of sequential machines/classic automata and the category of groupoids; therefore, one would be able to develop a homotopy theory of dynamic realisations of (M, R)-systems [20] based on dynamic realisations in a homotopy category, in a manner broadly similar to the development of the current Homotopy Theory for groupoids [12]-[13], including concepts such as the fundamental groupoid of a dynamic state space generated by any dynamic realisation of a simple (M, R)- system. Such dynamic realisations of (M, R)-systems can thus lead to higher homotopy and a Higher Dimensional Algebra of extended, or generalised (M, R)- systems that are endowed with dynamic, topological structures. ∎

On the other hand, *generalised* (M, R)-systems, or GMRs, can be constructed functorially by employing the Yoneda Lemma, as shown in refs.[4]-[5]; GMRs are no longer restricted to sets, and can be also endowed with *structure*, such as those possesed by quantum groupoids or quantum automata. It follows then immediately that, unless the structure of GMRs is restricted to that of quantum groupoids or quantum automata, the categories of quantum automata or quantum groupoids can be either isomorphic or equivalent only to a subcategory of the GMR category, C_{GMR}, and not to the category of all GMRs. A 'no-go' conjecture is then here proposed:

No-Go Conjecture for Recursive Computation of Generalised (M,R)–Systems. *The high level of complexity of generalised ($\boldsymbol{M},\boldsymbol{R}$)–Systems [5], [20] that represent functional (living) organisms in non-commutative modelling encoding diagrams [6],[10] prevents their complete computability via recursive programming functions or algorithms by either standard or quantum automata which require commutative encoding computation diagrams [9]–[10],[14].*

The concepts of quantum automata and quantum computation were initially studied, and are also currently further investigated, in the contexts of quantum genetics, genetic networks with nonlinear dynamics, and bioinformatics. In a previous publication [2]– after introducing the formal concept of quantum automaton–the possible implications of this concept for correctly modeling genetic and metabolic activities in functional (living) cells and organisms were also considered. This was followed by a formal report on quantum and abstract, symbolic computation based on the theory of categories, functors and natural transformations [3]. The notions of topological semigroup, quantum automaton, or quantum computer, were then suggested with

a view to their potential applications to the analogous simulation of biological systems, and especially genetic activities and nonlinear dynamics in genetic networks [6]–[7].

Further, detailed studies of nonlinear dynamics in genetic networks were carried out in categories of n-valued, Lukasiewicz Logic Algebras that showed significant dissimilarities [6] from the widespread Boolean models of human neural networks that may have begun with the early publication of [18]. Molecular models in terms of categories, functors and natural transformations were then formulated for uni-molecular chemical transformations, multi-molecular chemical and biochemical transformations [7]. Previous applications of computer modeling, classical automata theory, and relational biology to molecular biology, oncogenesis and medicine were extensively reviewed in a monograph [7], and several important conclusions were reached regarding both the potential and the limitations of computation-assisted modeling of biological systems, especially those concerned with very complex organisms such as *Homo sapiens sapiens* [7]– [10]. Computer modeling and recursive computation models are thus often restricted only to *compact* subsystems (see also the following **Compactness Lemma 1**) of complex living organisms that are represented by GMRs [4]- [5],[7].

Novel approaches to solving the realisation problems of Relational Biology models in Complex Systems Biology were introduced in terms of natural transformations between functors of such molecular categories. Several applications of such natural transformations of functors were then presented to protein biosynthesis, embryogenesis and nuclear transplant experiments. Other possible realisations in Molecular Biology and Relational Biology of organisms were then suggested in terms of quantum automata models in Quantum Genetics and Cellular Interactomics. Future developments of this novel approach are likely to also include: fuzzy relations in Biology and Epigenomics, Relational Biology modeling of complex immunological and hormonal regulatory systems, n-categories and *generalised LM*–Topoi of Lukasiewicz Logic Algebras and intuitionistic logic (Heyting) algebras for modeling nonlinear dynamics and cognitive processes in complex neural networks that are present in the human brain, as well as stochastic modeling of genetic networks in Lukasiewicz Logic Algebras (LLAs).

A special case of *compact* subsystems of a GMR representing some component of an organism, such as the skeleton, may however escape the interdiction imposed by the 'no-go' **Conjecture 2**. Such compact objects of a GMR–in the sense of category theory– form either an additive or an Abelian category $\mathcal{A}$ to which the following *compactness lemma* applies.

LEMMA 1.1

An object X in an Abelian category $\mathcal{A}$ with arbitrary direct sums (also called coproducts) is compact if and only if the functor $\hom_{\mathcal{A}}(X, -)$ commutes with

arbitrary direct sums, that is, if

$$\hom_{\mathcal{A}}(X, \bigoplus_{\alpha \in S} Y_\alpha) = \bigoplus_{\alpha \in S} \hom_{\mathcal{A}}(X, Y_\alpha). \tag{1.13}$$

(**Compactness Lemma** from ref. [21]).

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1.5 Metabolic-Replication Systems

Robert RosenRobertRosen introduced *metabolic–repair models*, or (M, R)-systems in mathematical biology (*abstract relational biology*) in 1957 ([26, 27]); such systems will be here abbreviated as MR-systems, (or simply MR's). Rosen, then represented the MR's in terms of categories of sets, deliberately selected without any structure other than the *discrete topology of sets*.

Theoreticians of life's origins postulate that Life on Earth has begun with the simplest possible organism, called the *primordial*. Mathematicians interested in biology and this important question of the minimal living organism have attempted to define the functional relations that would have made life possible in a such a minimal system– a grandad and granma of all living organisms on Earth.

DEFINITION 1.15 *The simplest MR-system* is a relational model of the primordial organism which is defined by the following categorical sequence (or diagram) of sets and set-theoretical mappings:

$$f : A \rightarrow B, \phi : B \rightarrow Hom_{MR}(A, B),$$

where A is the set of inputs to the MR-system, B is the set of its outputs, and ϕ is the 'repair map', or R-component, of the MR-system which associates to a certain product, or output b, the 'metabolic' component (such as an enzyme, E, for example) represented by the set-theoretical mapping f. Then, $Hom_{MR}(A, B)$ is defined as the set of all such metabolic (set-theoretical) mappings (occasionally written incorrectly by some authors as $\{f\}$).

DEFINITION 1.16

A general (M, R)-system was defined by Rosen (1958a,b) as the network or graph of the metabolic and repair components that were specified above in **Definition 1.15**; such components are networked in a complex, abstract 'organism' defined by all the abstract relations and connecting maps between

the sets specifying all the metabolic and repair components of such a general, abstract model of the biological organism. The mappings bettwen (M, R)-systems are defined as the the metabolic and repair set-theoretical mappings, such as f and ϕ (specified in **Definition 1.15**); moreover, there is also a finite number of sets (just like those that are defined as in **Definition 1.5**): A_i, B_i, whereas $f \in Hom_{MR_i}(A_i, B_i)$ and $\phi \in Hom_{MR_i}[B, Hom_{MR_i}(A_i, B_i)]$, with $i \in I$, and I being a finite index set, or directed set, with (f, ϕ) being a finite number of distinct metabolic and repair components pairs.

Alternatively, one may think of a a general MR-system as being 'made of' a finite number N of interconnected MR_i, metabolic-repair modules with input sets A_i and output sets B_i. To sum up: a *general MR-system* can be defined as a *family of interconnected quartets*: $\{(A_i, B_i, f_i, \phi_i)\}_{i \in I}$, where I is an index set of integers $i = 1, 2, ..., n$.

1.5.1   Category of (M,R)–systems

DEFINITION 1.17

A category of (M, R)-system quartet modules, $\{(A_i, B_i, f_i, \phi_i)\}_{i \in I}$, with I being an index set of integers $i = 1, 2, ..., n$, is a small category of sets with set-theoretical mappings defined by the MR-morphisms between the quarted modules $\{(A_i, B_i, f_i, \phi_i)\}_{i \in I}$, and also with repair components defined as $\phi_i \in Hom_{MR_i}[B, Hom_{MR_i}(A_i, B_i)]$, with the (M, R)-morphism composition defined by the usual composition of functions between sets.

With a few, additional notational changes it can be shown that the category of (M, R)-systems is a subcategory of the category of automata (or sequential machines), $\mathcal{S}_{[M,A]}$ ([30, 31]).

REMARK 1.7   For over two decades, Robert Rosen developed with several coworkers the MR-systems theory and its applications to life sciences, medicine and general systems theory. He also considered biocomplexity to be an 'emergent', defining feature of organisms which is *not reducible in terms of the molecular structures* (or molecular components) of the organism and their physicochemical interactions. However, in his last written book in 1997 on *"Essays on Life Itself", published posthumously in 2000*, Robert Rosen finally accepted the need for representing organisms in terms of *categories with structure* that entail biological functions, both metabolic and repair ones. Note also that, unlike Rashevsky in his theory of organismic sets, Rosen did not attempt to extend the MRs to modeling societies, even though with appropriate modifications of *generalized (M, R)-system categories with structure* ([30, 31, 36]), this is feasible and yields meaningful mathematical and sociological results. Thus, subsequent publications have generalized MR-system (GMRs) and have

studied the fundamental, mathematical properties of algebraic categories of GMRs that were constructed functorially based on the Yoneda-Grothendieck Lemma and construction. Then it was shown that such algebraic categories of GMRs are *Cartesian closed* [30]. Several *molecular biology realizations of GMRs* in terms of DNA, RNAs, enzymes, $RNA \rightarrow DNA$-reverse trancriptases, and other biomolecular components were subsequently introduced and discussed in ref. [44, 36, 37] in terms of *non-linear genetic network models* in many-valued, LM_n logic algebras (or the Algebraic Category of LM_n Logic Algebras).

If simple (M, R)-systems are considered as sequential machines or automata the category of (M, R)-systems and (M, R)-system homomorphisms is a subcategory of the automata category. However, when (M, R)-systems are considered together with their dynamic representations the category of dynamic (M, R)-systems is no longer a subcategory of the category of automata. ∎

1.6 The Category of Graphs (or Pseudographs)

. Realizations of Genetic and Neural Networks by Graphs with Variable Topology.

DEFINITION 1.18

A simple graph, $\mathcal{G}$ is an ordered pair of disjoint sets (N, E) of nodes $x \in N$ and edges $e_{xy} \in E$ such that E is a subset of the set $N^{(2)} = N \times N$ of unordered pairs of N. If the set N is finite then the graph $\mathcal{G}$ is also finite, as it is usually assumed with N and E being assumed to be finite, unless otherwise stated. The set N is the set of nodes, or *vertices*, and E is the set of *edges*.

Diagrams in a category can be considered as directed simple graphs in which the edges are replaced by arrows or morphisms that may satisfy commutativity:

$$
\begin{array}{ccc}
A & \overset{f}{\longrightarrow} & B \\
{\scriptstyle k}\downarrow & & \downarrow{\scriptstyle g} \\
C & \underset{h}{\longrightarrow} & D
\end{array}
$$

and identity conditions (or ETAC axioms).

DEFINITION 1.19

A pseudograph $\mathcal{G}_P$ is an ordered triple (V, E, i), where V is a set called the *vertex set* of $\mathcal{G}_P$, E is a set called the *edge set* of G, and $i : E \to 2^V$ is the *incidence map*, such that for every $e_i \in E$, $1 \leq |i(e)| \leq 2$.

REMARK 1.8   A pseudograph can be regarded as a generalization of the concept of graph. ∎

DEFINITION 1.20
For any two given pseudographs $G_{P1} = (V_1, E_1, i_1)$ and $G_{P2} = (V_2, E_2, i_2)$, *a graph homomorphism* $h : G_{P1} \to G_{P2}$ consists of two functions $f : V_1 \to V_2$ and $g : E_1 \to E_2$, such that

$$i_2 \circ g = f^* \circ i_1, \tag{1.14}$$

where the function $f^* : 2^{V_1} \to 2^{V_2}$ is defined as $f^*(S) = \{f(s) \mid s \in S\}$.

When $\mathcal{G}_1$ and $\mathcal{G}_2$ are just simple graphs, a graph homomorphism may be defined in terms of a single function $f : V_1 \to V_2$ satisfying the condition (*)

$\{v_1, v_2\}$ is an edge of $\mathcal{G}_1 \implies \{f(v_1), f(v_2)\}$ is an edge of $\mathcal{G}_2$.

A *graph isomorphism* $h = (f, g)$ is a graph homomorphism such that both f and g are bijections.
h is a *graph automorphism* if $\mathcal{G}_1 = \mathcal{G}_2$.

DEFINITION 1.21
The small category of graphs (or pseudographs*), G,* is a category whose objects are finite graphs (or pseudographs) and whose arrows are the graph (or, respectively, pseudograph) homomorphisms.

1.7   Conclusions

Non-distributive varieties of many-valued, LM-logic algebras that are also noncommutative open new possibilities for formal treatments of both complex quantum systems and highly complex biological networks, such as genetic nets, metabolic-replication systems (see for example refs. [19]–[20] and [22]), the interactome [6] and neural networks [7] in terms of quantum nano-automata operating on multi-scales. This novel approach that involves both Algebraic Logic and Category Theory, provides an important framework for understanding the complexity inherent in intelligent systems and their flexible, adaptive behaviors. A consequence of the Logical Adjointness Theorem–

which defines categorically the natural equivalence between the category of centered LM-logic algebras and that of Boolean logic algebras– is that one may be able to define Artificial Intelligence analogs of neural networks based on centered LM-logic algebras. In this process, higher dimensional algebra (HDA; [12]-[13]) and categorical models of human brain dynamics (refs. [8]–[11]) were predicted to play a central role. These new approaches are also relevant for resolving the tug-of-war between nature-vs.-nurture theories of human development and the 'natural' emergence through co-evolution of intelligence in the first *H. sapiens sapiens* societies.

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